

## SEQUENCE LISTING

<110> INCYTE PHARMACEUTICALS, INC.  
 BANDMAN, Olga  
 TANG, Y. Tom  
 YUE, Henry  
 CORLEY, Neil C.  
 GUEGLER, Karl J.  
 AZIMZAI, Yalda  
 PATTERSON, Chandra  
 LAL, Preeti  
 BAUGHN, Mariah R.

<120> HUMAN CYTOSKELETAL PROTEINS

<130> PF-0568 PCT

<140> To Be Assigned  
 <141> Herewith

<150> 09/127,665  
 <151> 1998-07-31

<160> 17

<170> PERL Program

<210> 1  
 <211> 284  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte Clone No: 1274060

<400> 1  
 Met Glu Ala Ile Lys Lys Lys Met Gln Met Leu Lys Leu Asp Lys  
 1 5 10 15  
 Glu Asn Ala Ile Asp Arg Ala Glu Gln Ala Glu Ala Asp Lys Lys  
 20 25 30  
 Ala Ala Glu Asp Lys Cys Lys Gln Val Glu Glu Glu Leu Thr His  
 35 40 45  
 Leu Gln Lys Leu Lys Gly Thr Glu Asp Glu Leu Asp Lys Tyr  
 50 55 60  
 Ser Glu Asp Leu Lys Asp Ala Gln Glu Lys Leu Glu Leu Thr Glu  
 65 70 75  
 Lys Lys Ala Ser Asp Ala Glu Gly Asp Val Ala Ala Leu Asn Arg  
 80 85 90  
 Arg Ile Gln Leu Val Glu Glu Glu Leu Asp Arg Ala Gln Glu Arg  
 95 100 105  
 Leu Ala Thr Ala Leu Gln Lys Leu Glu Glu Ala Glu Lys Ala Ala  
 110 115 120  
 Asp Glu Ser Glu Arg Gly Met Lys Val Ile Glu Asn Arg Ala Met  
 125 130 135  
 Lys Asp Glu Glu Lys Met Glu Ile Gln Glu Met Gln Leu Lys Glu  
 140 145 150  
 Ala Lys His Ile Ala Glu Glu Ala Asp Arg Lys Tyr Glu Glu Val  
 155 160 165  
 Ala Arg Lys Leu Val Ile Leu Glu Gly Glu Leu Glu Arg Ala Glu  
 170 175 180  
 Glu Arg Ala Glu Val Ser Glu Leu Lys Cys Gly Asp Leu Glu Glu  
 185 190 195

Glu	Leu	Lys	Asn	Val	Thr	Asn	Asn	Leu	Lys	Ser	Leu	Glu	Ala	Ala
200									205				210	
Ser	Glu	Lys	Tyr	Ser	Glu	Lys	Glu	Asp	Lys	Tyr	Glu	Glu	Ile	
215									220				225	
Lys	Leu	Leu	Ser	Asp	Lys	Leu	Lys	Glu	Ala	Glu	Thr	Arg	Ala	Glu
230									235				240	
Phe	Ala	Glu	Arg	Thr	Val	Ala	Lys	Leu	Glu	Lys	Thr	Ile	Asp	Asp
245									250				255	
Leu	Glu	Glu	Lys	Leu	Ala	Gln	Ala	Lys	Glu	Glu	Asn	Val	Gly	Leu
260									265				270	
His	Gln	Thr	Leu	Asp	Gln	Thr	Leu	Asn	Glu	Leu	Asn	Cys	Ile	
275									280					

<210> 2  
<211> 158  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> Incyte Clone No: 1577078

<400> 2  

Met	Lys	Val	Ile	Glu	Asn	Arg	Ala	Met	Lys	Asp	Glu	Glu	Lys	Met
1				5					10				15	
Glu	Ile	Gln	Glu	Met	Gln	Leu	Lys	Glu	Ala	Lys	His	Ile	Ala	Glu
				20					25				30	
Glu	Ala	Asp	Arg	Lys	Tyr	Glu	Glu	Val	Ala	Arg	Lys	Leu	Val	Ile
				35					40				45	
Leu	Glu	Gly	Glu	Leu	Glu	Arg	Ala	Glu	Glu	Arg	Ala	Glu	Val	Ser
				50					55				60	
Glu	Leu	Lys	Cys	Gly	Asp	Leu	Glu	Glu	Glu	Leu	Lys	Asn	Val	Thr
				65					70				75	
Asn	Asn	Leu	Lys	Ser	Leu	Glu	Ala	Ala	Ser	Glu	Lys	Tyr	Ser	Glu
				80					85				90	
Lys	Glu	Asp	Lys	Tyr	Glu	Glu	Glu	Ile	Lys	Leu	Leu	Ser	Asp	Lys
				95					100				105	
Leu	Lys	Glu	Ala	Glu	Thr	Arg	Ala	Glu	Phe	Ala	Glu	Arg	Thr	Val
				110					115				120	
Ala	Lys	Leu	Glu	Lys	Thr	Ile	Asp	Asp	Leu	Glu	Glu	Lys	Leu	Ala
				125					130				135	
Gln	Ala	Lys	Glu	Glu	Asn	Val	Gly	Leu	His	Gln	Thr	Leu	Asp	Gln
				140					145				150	
Thr	Leu	Asn	Glu	Leu	Asn	Cys	Ile							
				155										

<210> 3  
<211> 208  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> Incyte Clone No: 1426711

<400> 3

Met	Asp	Ala	Ile	Lys	Lys	Met	Gln	Met	Leu	Lys	Leu	Asp	Lys
1				5				10					15
Glu	Asn	Ala	Leu	Asp	Arg	Ala	Glu	Gln	Ala	Glu	Ala	Asp	Lys
				20				25					30
Ala	Ala	Glu	Asp	Arg	Ser	Lys	Gln	Leu	Glu	Glu	Asp	Ile	Ala
				35				40					45
Lys	Glu	Lys	Leu	Leu	Arg	Val	Ser	Glu	Asp	Glu	Arg	Asp	Arg
				50				55					60
Leu	Glu	Glu	Leu	His	Lys	Ala	Glu	Asp	Ser	Leu	Leu	Ala	Glu
				65				70					75
Glu	Ala	Ala	Ala	Lys	Ala	Glu	Ala	Asp	Val	Ala	Ser	Leu	Asn
				80				85					90
Arg	Ile	Gln	Leu	Val	Glu	Glu	Glu	Leu	Asp	Arg	Ala	Gln	Glu
				95				100					105
Leu	Ala	Thr	Ala	Leu	Gln	Lys	Leu	Glu	Glu	Ala	Glu	Lys	Ala
				110				115					120
Asp	Glu	Ser	Glu	Arg	Gly	Met	Lys	Val	Ile	Glu	Ser	Arg	Ala
				125				130					135
Lys	Asp	Glu	Glu	Lys	Met	Glu	Ile	Gln	Glu	Ile	Gln	Leu	Glu
				140				145					150
Ala	Lys	His	Ile	Ala	Glu	Asp	Ala	Asp	Arg	Lys	Tyr	Glu	Val
				155				160					165
Ala	Arg	Lys	Leu	Val	Ile	Ile	Glu	Ser	Asp	Leu	Glu	Arg	Ala
				170				175					180
Glu	Arg	Ala	Gly	Glu	Gly	Leu	Asp	Lys	Asp	Arg	Arg	Ala	Ala
				185				190					195
His	His	Pro	Ser	Pro	His	Pro	His	Pro	Leu	Leu	Glu	Phe	
				200				205					

<210> 4  
<211> 156  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> Incyte Clone No: 1676756

Met	Ile	Lys	Arg	Val	Leu	Leu	Glu	Arg	Leu	Glu	Asn	Thr	Arg	Lys
1				5				10						15
Leu	Arg	Glu	Leu	Thr	Glu	Gly	Arg	Thr	Leu	Asp	Trp	Pro	Gln	Asn
				20				25						30
Arg	Ile	Thr	Glu	Val	Ser	Ala	Lys	Arg	Gln	Ile	Val	Thr	Glu	Tyr
				35				40						45
Arg	Glu	Lys	Gly	Lys	Arg	Asn	Tyr	Glu	Glu	Lys	Lys	Arg	Asp	Leu
				50				55						60
Glu	Gly	Arg	Ser	Arg	Arg	Tyr	Asn	Leu	Cys	Ile	Ile	Gly	Ile	Pro
				65				70						75
Glu	Thr	Glu	Asp	Arg	Ala	Ser	Gly	Ala	Glu	Thr	Ile	Lys	Asp	Leu
				80				85						90
Leu	Glu	Lys	Asn	Phe	Pro	Glu	Leu	Lys	Asn	Glu	Leu	Asp	Leu	Gln
				95				100						105
Met	Glu	Lys	Ala	His	Arg	Ile	Pro	Leu	Lys	Phe	Asn	Glu	Lys	Lys
				110				115						120
Ala	Ala	Ser	Arg	His	Ile	Arg	Val	Thr	Phe	Leu	Asn	Phe	Lys	Asp
				125				130						135
Glu	Thr	Phe	Tyr	Lys	His	Pro	Val	Arg	Glu	Ser	Arg	Leu	Leu	Thr
				140				145						150
Lys	Gly	Gln	Lys	Ser	Gly									
				155										

<210> 5  
<211> 876  
<212> PRT  
<213> *Homo sapiens*

<220>  
<221> misc\_feature  
<223> Incyte Clone No: 1843770

<400> 5  
 Met Ala Ser Asp Ala Ser His Ala Leu Glu Ala Ala Leu Glu Gln  
 1 5 10 15  
 Met Asp Gly Ile Ile Ala Gly Thr Lys Thr Gly Ala Asp Leu Ser  
 20 25 30  
 Asp Gly Thr Cys Glu Pro Gly Leu Ala Ser Pro Ala Ser Tyr Met  
 35 40 45  
 Asn Pro Phe Pro Val Leu His Leu Ile Glu Asp Leu Arg Leu Ala  
 50 55 60  
 Leu Glu Met Leu Glu Leu Pro Gln Glu Arg Ala Ala Leu Leu Ser  
 65 70 75  
 Gln Ile Pro Gly Pro Thr Ala Ala Tyr Ile Lys Glu Trp Phe Glu  
 80 85 90  
 Glu Ser Leu Ser Gln Val Asn His His Ser Ala Ala Ser Asn Glu  
 95 100 105  
 Thr Tyr Gln Glu Arg Leu Ala Arg Leu Glu Gly Asp Lys Glu Ser  
 110 115 120  
 Leu Ile Leu Gln Val Ser Val Leu Thr Asp Gln Val Glu Ala Gln  
 125 130 135  
 Gly Glu Lys Ile Arg Asp Leu Glu Val Cys Leu Glu Gly His Gln  
 140 145 150  
 Val Lys Leu Asn Ala Ala Glu Glu Met Leu Gln Gln Glu Leu Leu  
 155 160 165  
 Ser Arg Thr Ser Leu Glu Thr Gln Lys Leu Asp Leu Met Thr Glu  
 170 175 180  
 Val Ser Glu Leu Lys Leu Lys Leu Val Gly Met Glu Lys Glu Gln  
 185 190 195  
 Arg Glu Gln Glu Glu Lys Gln Arg Lys Ala Glu Glu Leu Leu Gln  
 200 205 210  
 Glu Leu Arg His Leu Lys Ile Lys Val Glu Glu Leu Glu Asn Glu  
 215 220 225  
 Arg Asn Gln Tyr Glu Trp Lys Leu Lys Ala Thr Lys Ala Glu Val  
 230 235 240  
 Ala Gln Leu Gln Glu Gln Val Ala Leu Lys Asp Ala Glu Ile Glu  
 245 250 255  
 Arg Leu His Ser Gln Leu Ser Arg Thr Ala Ala Leu His Ser Glu  
 260 265 270  
 Ser His Thr Glu Arg Asp Gln Glu Ile Gln Arg Leu Lys Met Gly  
 275 280 285  
 Met Glu Thr Leu Leu Leu Ala Asn Glu Asp Lys Asp Arg Arg Ile  
 290 295 300  
 Glu Glu Leu Thr Gly Leu Leu Asn Gln Tyr Arg Lys Val Lys Glu  
 305 310 315  
 Ile Val Met Val Thr Gln Gly Pro Ser Glu Arg Thr Leu Ser Ile  
 320 325 330  
 Asn Glu Glu Glu Pro Glu Gly Gly Phe Ser Lys Trp Asn Ala Thr  
 335 340 345  
 Asn Lys Asp Pro Glu Glu Leu Phe Lys Gln Glu Met Pro Pro Arg  
 350 355 360  
 Cys Ser Ser Pro Thr Val Gly Pro Pro Pro Leu Pro Gln Lys Ser  
 365 370 375  
 Leu Glu Thr Arg Ala Gln Lys Lys Leu Ser Cys Ser Leu Glu Asp  
 380 385 390  
 Leu Arg Ser Glu Ser Val Asp Lys Cys Met Asp Gly Asn Gln Pro  
 395 400 405

Phe	Pro	Val	Leu	Glu	Pro	Lys	Asp	Ser	Pro	Phe	Leu	Ala	Glu	His
410									415					420
Lys	Tyr	Pro	Thr	Leu	Pro	Gly	Lys	Leu	Ser	Gly	Ala	Thr	Pro	Asn
425									430					435
Gly	Glu	Ala	Ala	Lys	Ser	Pro	Pro	Thr	Ile	Cys	Gln	Pro	Asp	Ala
440									445					450
Thr	Gly	Ser	Ser	Leu	Leu	Arg	Leu	Arg	Asp	Thr	Glu	Ser	Gly	Trp
455									460					465
Asp	Asp	Thr	Ala	Val	Val	Asn	Asp	Leu	Ser	Ser	Thr	Ser	Ser	Gly
470									475					480
Thr	Glu	Ser	Gly	Pro	Gln	Ser	Pro	Leu	Thr	Pro	Asp	Gly	Lys	Arg
485									490					495
Asn	Pro	Lys	Gly	Ile	Lys	Lys	Phe	Trp	Gly	Lys	Ile	Arg	Arg	Thr
500									505					510
Gln	Ser	Gly	Asn	Phe	Tyr	Thr	Asp	Thr	Leu	Gly	Met	Ala	Glu	Phe
515									520					525
Arg	Arg	Gly	Gly	Leu	Arg	Ala	Thr	Ala	Gly	Pro	Arg	Leu	Ser	Arg
530									535					540
Thr	Arg	Asp	Ser	Lys	Gly	Gln	Lys	Ser	Asp	Ala	Asn	Ala	Pro	Phe
545									550					555
Ala	Gln	Trp	Ser	Thr	Glu	Arg	Val	Cys	Ala	Trp	Leu	Glu	Asp	Phe
560									565					570
Gly	Leu	Ala	Gln	Tyr	Val	Ile	Phe	Ala	Arg	Gln	Trp	Val	Ser	Ser
575									580					585
Gly	His	Thr	Leu	Leu	Thr	Ala	Thr	Pro	Gln	Asp	Met	Glu	Lys	Glu
590									595					600
Leu	Gly	Ile	Lys	His	Pro	Leu	His	Arg	Lys	Lys	Leu	Val	Leu	Ala
605									610					615
Val	Lys	Ala	Ile	Asn	Thr	Lys	Gln	Glu	Glu	Lys	Ser	Ala	Leu	Leu
620									625					630
Asp	His	Ile	Trp	Val	Thr	Arg	Trp	Leu	Asp	Asp	Ile	Gly	Leu	Pro
635									640					645
Gln	Tyr	Lys	Asp	Gln	Phe	His	Glu	Ser	Arg	Val	Asp	Gly	Arg	Met
650									655					660
Leu	Gln	Tyr	Leu	Thr	Val	Asn	Asp	Leu	Leu	Phe	Leu	Lys	Val	Thr
665									670					675
Ser	Gln	Leu	His	His	Leu	Ser	Ile	Lys	Cys	Ala	Ile	His	Val	Leu
680									685					690
His	Val	Asn	Lys	Phe	Asn	Pro	His	Cys	Leu	His	Arg	Arg	Pro	Ala
695									700					705
Asp	Glu	Ser	Asn	Leu	Ser	Pro	Ser	Glu	Val	Val	Gln	Trp	Ser	Asn
710									715					720
His	Arg	Val	Met	Glu	Trp	Leu	Arg	Ser	Val	Asp	Leu	Ala	Glu	Tyr
725									730					735
Ala	Pro	Asn	Leu	Arg	Gly	Ser	Gly	Val	His	Gly	Gly	Leu	Ile	Ile
740									745					750
Leu	Glu	Pro	Arg	Phe	Thr	Gly	Asp	Thr	Leu	Ala	Met	Leu	Leu	Asn
755									760					765
Ile	Pro	Pro	Gln	Lys	Thr	Leu	Leu	Arg	Arg	His	Leu	Thr	Thr	Lys
770									775					780
Phe	Asn	Ala	Leu	Ile	Gly	Pro	Glu	Ala	Glu	Gln	Glu	Lys	Arg	Glu
785									790					795
Lys	Met	Ala	Ser	Pro	Ala	Tyr	Thr	Pro	Leu	Thr	Thr	Thr	Ala	Lys
800									805					810
Val	Arg	Pro	Arg	Lys	Leu	Gly	Phe	Ser	His	Phe	Gly	Asn	Ile	Arg
815									820					825
Lys	Lys	Lys	Phe	Asp	Glu	Ser	Thr	Asp	Tyr	Ile	Cys	Pro	Met	Glu
830									835					840
Pro	Ser	Asp	Gly	Val	Ser	Asp	Ser	His	Arg	Val	Tyr	Ser	Gly	Tyr
845									850					855
Arg	Gly	Leu	Ser	Pro	Leu	Asp	Ala	Pro	Glu	Leu	Asp	Gly	Leu	Asp
860									865					870
Gln	Val	Gly	Gln	Ile	Ser									
875														

<210> 6  
<211> 806  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc feature  
<223> Incyte Clone No: 3768043

<400> 6  
Met Glu Glu Pro Gly Ala Thr Pro Gln Pro Tyr Leu Gly Leu Val  
1 5 10 15  
Leu Glu Glu Leu Arg Arg Val Val Ala Ala Leu Pro Glu Ser Met  
20 25 30  
Arg Pro Asp Glu Asn Pro Tyr Gly Phe Pro Ser Glu Leu Val Val  
35 40 45  
Cys Ala Ala Val Ile Gly Phe Phe Val Val Leu Leu Phe Leu Trp  
50 55 60  
Arg Ser Phe Arg Ser Val Arg Ser Arg Leu Tyr Val Gly Arg Glu  
65 70 75  
Gln Lys Leu Gly Ala Thr Leu Ser Gly Leu Ile Glu Glu Lys Cys  
80 85 90  
Lys Leu Leu Glu Lys Phe Ser Leu Ile Gln Lys Glu Tyr Glu Gly  
95 100 105  
Tyr Glu Val Glu Ser Ser Leu Glu Asp Ala Ser Phe Glu Lys Glu  
110 115 120  
Ala Ala Glu Glu Ala Arg Ser Leu Glu Ala Thr Cys Glu Lys Leu  
125 130 135  
Asn Arg Ser Asn Ser Glu Leu Glu Asp Glu Ile Leu Cys Leu Glu  
140 145 150  
Lys Asp Leu Lys Gln Glu Lys Ser Lys His Ser Gln Gln Asp Glu  
155 160 165  
Leu Met Ala Asp Ile Ser Lys Ser Ile Gln Ser Leu Glu Asp Glu  
170 175 180  
Ser Lys Ser Leu Lys Ser Gln Ile Ala Glu Ala Lys Ile Ile Cys  
185 190 195  
Lys Thr Phe Lys Met Ser Glu Glu Arg Arg Ala Ile Ala Ile Lys  
200 205 210  
Asp Ala Leu Asn Glu Asn Ser Gln Leu Gln Thr Ser His Lys Gln  
215 220 225  
Leu Phe Gln Gln Glu Ala Glu Val Trp Lys Gly Glu Val Ser Glu  
230 235 240  
Leu Asn Lys Gln Lys Ile Thr Phe Glu Asp Ser Lys Val His Ala  
245 250 255  
Glu Gln Val Leu Asn Asp Lys Glu Asn His Ile Lys Thr Leu Thr  
260 265 270  
Gly His Leu Pro Met Met Lys Asp Gln Ala Ala Val Leu Glu Glu  
275 280 285  
Asp Thr Thr Asp Asp Asp Asn Leu Glu Leu Glu Val Asn Ser Glu  
290 295 300  
Ser Glu Asn Gly Ala Tyr Leu Asp Asn Pro Pro Lys Gly Ala Leu  
305 310 315  
Lys Lys Leu Ile His Ala Ala Lys Leu Asn Ala Ser Leu Lys Thr  
320 325 330  
Leu Glu Gly Glu Arg Asn Gln Ile Tyr Ile Gln Leu Ser Glu Val  
335 340 345  
Asp Lys Thr Lys Glu Glu Leu Thr Glu His Ile Lys Asn Leu Gln  
350 355 360  
Thr Gln Gln Ala Ser Leu Gln Ser Glu Asn Thr His Phe Glu Asn  
365 370 375  
Glu Asn Gln Lys Leu Gln Gln Lys Leu Lys Val Met Thr Glu Leu  
380 385 390

Tyr Gln Glu Asn Glu Met Lys Leu His Arg Lys Leu Thr Val Glu  
 395 400 405  
 Glu Asn Tyr Arg Leu Glu Lys Glu Glu Lys Leu Ser Lys Val Asp  
 410 415 420  
 Glu Lys Ile Ser His Ala Thr Glu Glu Leu Glu Thr Tyr Arg Lys  
 425 430 435  
 Arg Ala Lys Asp Leu Glu Glu Leu Glu Arg Thr Ile His Ser  
 440 445 450  
 Tyr Gln Gly Gln Ile Ile Ser His Glu Lys Lys Ala His Asp Asn  
 455 460 465  
 Trp Leu Ala Ala Arg Asn Ala Glu Arg Asn Leu Asn Asp Leu Arg  
 470 475 480  
 Lys Glu Asn Ala His Asn Arg Gln Lys Leu Thr Glu Thr Glu Leu  
 485 490 495  
 Lys Phe Glu Leu Leu Glu Lys Asp Pro Tyr Ala Leu Asp Val Pro  
 500 505 510  
 Asn Thr Ala Phe Gly Arg Glu His Ser Pro Tyr Gly Pro Ser Pro  
 515 520 525  
 Leu Gly Trp Pro Ser Ser Glu Thr Arg Ala Phe Leu Ser Pro Pro  
 530 535 540  
 Thr Leu Leu Glu Gly Pro Leu Arg Leu Ser Pro Leu Leu Pro Gly  
 545 550 555  
 Gly Gly Gly Arg Gly Ser Arg Gly Pro Gly Asn Pro Leu Asp His  
 560 565 570  
 Gln Ile Thr Asn Glu Arg Gly Glu Ser Ser Cys Asp Arg Leu Thr  
 575 580 585  
 Asp Pro His Arg Ala Pro Ser Asp Thr Gly Ser Leu Ser Pro Pro  
 590 595 600  
 Trp Asp Gln Asp Arg Arg Met Met Phe Pro Pro Pro Gly Gln Ser  
 605 610 615  
 Tyr Pro Asp Ser Ala Leu Pro Pro Gln Arg Gln Asp Arg Phe Cys  
 620 625 630  
 Ser Asn Ser Gly Arg Leu Ser Gly Pro Ala Glu Leu Arg Ser Phe  
 635 640 645  
 Asn Met Pro Ser Leu Asp Lys Met Asp Gly Ser Met Pro Ser Glu  
 650 655 660  
 Met Glu Ser Ser Arg Asn Asp Thr Lys Asp Asp Leu Gly Asn Leu  
 665 670 675  
 Asn Val Pro Asp Ser Ser Leu Pro Ala Glu Asn Glu Ala Thr Gly  
 680 685 690  
 Pro Gly Phe Val Pro Pro Pro Leu Ala Pro Ile Arg Gly Pro Leu  
 695 700 705  
 Phe Pro Val Asp Ala Arg Gly Pro Phe Leu Arg Arg Gly Pro Pro  
 710 715 720  
 Phe Pro Pro Pro Pro Pro Gly Ala Met Phe Gly Ala Ser Arg Asp  
 725 730 735  
 Tyr Phe Pro Pro Arg Asp Phe Pro Gly Pro Pro Pro Ala Pro Phe  
 740 745 750  
 Ala Met Arg Asn Val Tyr Pro Pro Arg Gly Phe Pro Pro Tyr Leu  
 755 760 765  
 Pro Pro Arg Pro Gly Phe Phe Pro Pro Pro Pro His Ser Glu Gly  
 770 775 780  
 Arg Ser Glu Phe Pro Ser Gly Leu Ile Pro Pro Ser Asn Glu Pro  
 785 790 795  
 Ala Thr Glu His Pro Glu Pro Gln Gln Glu Thr  
 800 805

<210> 7  
 <211> 2442  
 <212> PRT  
 <213> Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;223&gt; Incyte Clone No: 1655208

&lt;400&gt; 7

Met	Glu	Thr	Arg	Ser	Pro	Gly	Leu	Asn	Asn	Met	Lys	Pro	Gln	Ser
1				5				10					15	
Leu	Gln	Leu	Val	Leu	Glu	Glu	Gln	Val	Leu	Ala	Leu	Gln	Gln	Gln
					20				25				30	
Met	Ala	Glu	Asn	Gln	Ala	Ala	Ser	Trp	Arg	Lys	Leu	Lys	Asn	Ser
					35				40				45	
Gln	Glu	Ala	Gln	Gln	Arg	Gln	Ala	Thr	Leu	Val	Arg	Lys	Leu	Gln
					50				55				60	
Ala	Lys	Val	Leu	Gln	Tyr	Arg	Ser	Trp	Cys	Gln	Glu	Leu	Glu	Lys
					65				70				75	
Arg	Leu	Glu	Ala	Thr	Gly	Gly	Pro	Ile	Pro	Gln	Arg	Trp	Glu	Asn
					80				85				90	
Val	Glu	Glu	Pro	Asn	Leu	Asp	Glu	Leu	Leu	Val	Arg	Leu	Glu	Glu
					95				100				105	
Glu	Gln	Gln	Arg	Cys	Glu	Ser	Leu	Ala	Glu	Val	Asn	Thr	Gln	Ile
					110				115				120	
Arg	Leu	His	Met	Glu	Lys	Ala	Asp	Val	Val	Asn	Lys	Ala	Leu	Arg
					125				130				135	
Ala	Asp	Val	Glu	Lys	Leu	Thr	Val	Asp	Trp	Ser	Arg	Ala	Arg	Asp
					140				145				150	
Glu	Leu	Met	Arg	Lys	Glu	Ser	Gln	Trp	Gln	Met	Glu	Gln	Glu	Phe
					155				160				165	
Phe	Lys	Gly	Tyr	Leu	Lys	Gly	Glu	His	Gly	Arg	Leu	Leu	Ser	Leu
					170				175				180	
Trp	Arg	Glu	Val	Val	Thr	Phe	Arg	Arg	His	Phe	Leu	Glu	Met	Lys
					185				190				195	
Ser	Ala	Thr	Asp	Arg	Asp	Leu	Met	Glu	Leu	Lys	Ala	Glu	His	Val
					200				205				210	
Arg	Leu	Ser	Gly	Ser	Leu	Leu	Thr	Cys	Cys	Leu	Arg	Leu	Thr	Val
					215				220				225	
Gly	Ala	Gln	Ser	Arg	Glu	Pro	Asn	Gly	Ser	Gly	Arg	Met	Asp	Gly
					230				235				240	
Arg	Glu	Pro	Ala	Gln	Leu	Leu	Leu	Leu	Leu	Ala	Lys	Thr	Gln	Glu
					245				250				255	
Leu	Glu	Lys	Glu	Ala	His	Glu	Arg	Ser	Gln	Glu	Ile	Gln	Leu	
					260				265				270	
Lys	Ser	Gln	Gly	Asp	Leu	Glu	Lys	Ala	Glu	Leu	Gln	Asp	Arg	Val
					275				280				285	
Thr	Glu	Leu	Ser	Ala	Leu	Leu	Thr	Gln	Ser	Gln	Lys	Gln	Asn	Glu
					290				295				300	
Asp	Tyr	Glu	Lys	Met	Ile	Lys	Ala	Leu	Arg	Glu	Thr	Val	Glu	Ile
					305				310				315	
Leu	Glu	Thr	Asn	His	Thr	Glu	Leu	Met	Glu	His	Glu	Ala	Ser	Leu
					320				325				330	
Ser	Arg	Asn	Ala	Gln	Glu	Glu	Lys	Leu	Ser	Leu	Gln	Gln	Val	Ile
					335				340				345	
Lys	Asp	Ile	Thr	Gln	Val	Met	Val	Glu	Glu	Gly	Asp	Asn	Ile	Ala
					350				355				360	
Gln	Gly	Ser	Gly	Leu	Glu	Asn	Ser	Leu	Glu	Leu	Glu	Ser	Ser	Ile
					365				370				375	
Phe	Ser	Gln	Phe	Asp	Tyr	Gln	Asp	Ala	Asp	Lys	Ala	Leu	Thr	Leu
					380				385				390	
Val	Arg	Ser	Val	Leu	Thr	Arg	Arg	Arg	Gln	Ala	Val	Gln	Asp	Leu
					395				400				405	
Arg	Gln	Gln	Leu	Ala	Gly	Cys	Gln	Glu	Ala	Val	Asn	Leu	Gln	
					410				415				420	
Gln	Gln	His	Asp	Gln	Trp	Glu	Glu	Gly	Lys	Ala	Leu	Arg	Gln	
					425				430				435	
Arg	Leu	Gln	Lys	Leu	Thr	Gly	Glu	Arg	Asp	Thr	Leu	Ala	Gly	Gln
					440				445				450	

Thr Val Asp Leu Gln Gly Glu Val Asp Ser Leu Ser Lys Glu Arg  
455 460 465  
Glu Leu Leu Gln Lys Ala Arg Glu Glu Leu Arg Gln Gln Leu Glu  
470 475 480  
Val Leu Glu Gln Glu Ala Trp Arg Leu Arg Arg Val Asn Val Glu  
485 490 495  
Leu Gln Leu Gln Gly Asp Ser Ala Gln Gly Gln Lys Glu Glu Gln  
500 505 510  
Gln Glu Glu Leu His Leu Ala Val Arg Glu Arg Glu Arg Leu Gln  
515 520 525  
Glu Met Leu Met Gly Leu Glu Ala Lys Gln Ser Glu Ser Leu Ser  
530 535 540  
Glu Leu Ile Thr Leu Arg Glu Ala Leu Glu Ser Ile His Leu Glu  
545 550 555  
Gly Glu Leu Leu Arg Gln Glu Gln Thr Glu Val Thr Ala Ala Leu  
560 565 570  
Ala Arg Ala Glu Gln Ser Ile Ala Glu Leu Ser Ser Ser Glu Asn  
575 580 585  
Thr Leu Lys Thr Glu Val Ala Asp Leu Arg Ala Ala Ala Val Lys  
590 595 600  
Leu Ser Ala Leu Asn Glu Ala Leu Ala Leu Asp Lys Val Gly Leu  
605 610 615  
Asn Gln Gln Leu Leu Gln Leu Glu Glu Glu Asn Gln Ser Val Cys  
620 625 630  
Ser Arg Met Glu Ala Ala Glu Gln Ala Arg Asn Ala Leu Gln Val  
635 640 645  
Asp Leu Ala Glu Ala Glu Lys Arg Arg Glu Ala Leu Trp Glu Lys  
650 655 660  
Asn Thr His Leu Glu Ala Gln Leu Gln Lys Ala Glu Glu Ala Gly  
665 670 675  
Ala Glu Leu Gln Ala Asp Leu Arg Asp Ile Gln Glu Glu Lys Glu  
680 685 690  
Glu Ile Gln Lys Lys Leu Ser Glu Ser Arg His Gln Gln Glu Ala  
695 700 705  
Ala Thr Thr Gln Leu Glu Gln Leu His Gln Glu Ala Lys Arg Gln  
710 715 720  
Glu Glu Val Leu Ala Arg Ala Val Gln Glu Lys Glu Ala Leu Val  
725 730 735  
Arg Glu Lys Ala Ala Leu Glu Val Arg Leu Gln Ala Val Glu Arg  
740 745 750  
Asp Arg Gln Asp Leu Ala Ala Gln Leu Gln Gly Leu Ser Ser Ala  
755 760 765  
Lys Glu Leu Leu Glu Ser Ser Leu Phe Glu Ala Gln Gln Gln Asn  
770 775 780  
Ser Val Ile Asp Glu Pro Gln Gly Gln Leu Glu Val Gln Ile Gln  
785 790 795  
Thr Val Thr Gln Ala Lys Glu Val Ile Gln Gly Glu Val Arg Cys  
800 805 810  
Leu Lys Leu Glu Leu Asp Thr Glu Arg Ser Gln Ala Glu Gln Glu  
815 820 825  
Arg Asp Ala Ala Ala Arg Gln Leu Ala Gln Ala Glu Gln Glu Gly  
830 835 840  
Lys Thr Ala Leu Glu Gln Gln Lys Ala Ala His Glu Lys Glu Val  
845 850 855  
Asn Gln Leu Arg Glu Lys Trp Glu Lys Glu Arg Ser Trp His Gln  
860 865 870  
Gln Glu Leu Ala Lys Ala Leu Glu Ser Leu Glu Arg Glu Lys Met  
875 880 885  
Glu Leu Glu Met Arg Leu Lys Glu Gln Gln Thr Glu Met Glu Ala  
890 895 900  
Ile Gln Ala Gln Arg Glu Glu Glu Arg Thr Gln Ala Glu Ser Ala  
905 910 915  
Leu Cys Gln Met Gln Leu Glu Thr Glu Lys Glu Arg Val Ser Leu  
920 925 930  
Leu Glu Thr Leu Leu Gln Thr Gln Lys Glu Leu Ala Asp Ala Ser

935	940	945
Gln Gln Leu Glu Arg Leu Arg Gln Asp	Met Lys Val Gln Lys Leu	
950	955	960
Lys Glu Gln Glu Thr Thr Gly Ile Leu Gln Thr Gln Leu Gln Glu		
965	970	975
Ala Gln Arg Glu Leu Lys Glu Ala Ala Arg Gln His Arg Asp Asp		
980	985	990
Leu Ala Ala Leu Gln Glu Glu Ser Ser Leu Leu Gln Asp Lys		
995	1000	1005
Met Asp Leu Gln Lys Gln Val Glu Asp Leu Lys Ser Gln Leu Val		
1010	1015	1020
Ala Gln Asp Asp Ser Gln Arg Leu Val Glu Gln Glu Val Gln Glu		
1025	1030	1035
Lys Leu Arg Glu Thr Gln Glu Tyr Asn Arg Ile Gln Lys Glu Leu		
1040	1045	1050
Glu Arg Glu Lys Ala Ser Leu Thr Leu Ser Leu Met Glu Lys Glu		
1055	1060	1065
Gln Arg Leu Leu Val Leu Gln Glu Ala Asp Ser Ile Arg Gln Gln		
1070	1075	1080
Glu Leu Ser Ala Leu Arg Gln Asp Met Gln Glu Ala Gln Gly Glu		
1085	1090	1095
Gln Lys Glu Leu Ser Ala Gln Met Glu Leu Leu Arg Gln Glu Val		
1100	1105	1110
Lys Glu Lys Glu Ala Asp Phe Leu Ala Gln Glu Ala Gln Leu Leu		
1115	1120	1125
Glu Glu Leu Glu Ala Ser His Ile Thr Glu Gln Gln Leu Arg Ala		
1130	1135	1140
Ser Leu Trp Ala Gln Glu Ala Lys Ala Ala Gln Leu His Leu Arg		
1145	1150	1155
Leu Arg Ser Thr Glu Ser Gln Leu Glu Ala Leu Ala Ala Glu Gln		
1160	1165	1170
Gln Pro Gly Asn Gln Ala Gln Ala Gln Ala Gln Leu Ala Ser Leu		
1175	1180	1185
Tyr Ser Ala Leu Gln Gln Ala Leu Gly Ser Val Cys Glu Ser Arg		
1190	1195	1200
Pro Glu Leu Ser Gly Gly Asp Ser Ala Pro Ser Val Trp Gly		
1205	1210	1215
Leu Glu Pro Asp Gln Asn Gly Ala Arg Ser Leu Phe Lys Arg Gly		
1220	1225	1230
Pro Leu Leu Thr Ala Leu Ser Ala Glu Ala Val Ala Ser Ala Leu		
1235	1240	1245
Leu Lys Leu His Gln Asp Leu Trp Lys Thr Gln Gln Thr Arg Asp		
1250	1255	1260
Val Leu Arg Asp Gln Val Gln Lys Leu Glu Glu Arg Leu Thr Asp		
1265	1270	1275
Thr Glu Ala Glu Lys Ser Gln Val His Thr Glu Leu Gln Asp Leu		
1280	1285	1290
Gln Arg Gln Leu Ser Gln Asn Gln Glu Glu Lys Ser Lys Trp Glu		
1295	1300	1305
Gly Lys Gln Asn Ser Leu Glu Ser Glu Leu Met Glu Leu His Glu		
1310	1315	1320
Thr Met Ala Ser Leu Gln Ser Arg Leu Arg Arg Ala Glu Leu Gln		
1325	1330	1335
Arg Met Glu Ala Gln Gly Glu Arg Glu Leu Leu Gln Ala Ala Lys		
1340	1345	1350
Glu Asn Leu Thr Ala Gln Val Glu His Leu Gln Ala Ala Val Val		
1355	1360	1365
Glu Ala Arg Ala Gln Ala Ser Ala Ala Gly Ile Leu Glu Glu Asp		
1370	1375	1380
Leu Arg Thr Ala Arg Ser Ala Leu Lys Leu Lys Asn Glu Glu Val		
1385	1390	1395
Glu Ser Glu Arg Glu Arg Ala Gln Ala Leu Gln Glu Gln Gly Glu		
1400	1405	1410
Leu Lys Val Ala Gln Gly Lys Ala Leu Gln Glu Asn Leu Ala Leu		
1415	1420	1425

Leu Thr Gln Thr Leu Ala Glu Arg Glu Glu Glu Val Glu Thr Leu  
1430 1435 1440  
Arg Gly Gln Ile Gln Glu Leu Glu Lys Gln Arg Glu Met Gln Lys  
1445 1450 1455  
Ala Ala Leu Glu Leu Leu Ser Leu Asp Leu Lys Lys Arg Asn Gln  
1460 1465 1470  
Glu Val Asp Leu Gln Glu Gln Ile Gln Glu Leu Glu Lys Cys  
1475 1480 1485  
Arg Ser Val Leu Glu His Leu Pro Met Ala Val Gln Glu Arg Glu  
1490 1495 1500  
Gln Lys Leu Thr Val Gln Arg Glu Gln Ile Arg Glu Leu Glu Lys  
1505 1510 1515  
Asp Arg Glu Thr Gln Arg Asn Val Leu Glu His Gln Leu Leu Glu  
1520 1525 1530  
Leu Glu Lys Lys Asp Gln Met Ile Glu Ser Gln Arg Gly Gln Val  
1535 1540 1545  
Gln Asp Leu Lys Lys Gln Leu Val Thr Leu Glu Cys Leu Ala Leu  
1550 1555 1560  
Glu Leu Glu Glu Asn His His Lys Met Glu Cys Gln Gln Lys Leu  
1565 1570 1575  
Ile Lys Glu Leu Glu Gly Gln Arg Glu Thr Gln Arg Val Ala Leu  
1580 1585 1590  
Thr His Leu Thr Leu Asp Leu Glu Glu Arg Ser Gln Glu Leu Gln  
1595 1600 1605  
Ala Gln Ser Ser Gln Ile His Asp Leu Glu Ser His Ser Thr Val  
1610 1615 1620  
Leu Ala Arg Glu Leu Gln Glu Arg Asp Gln Glu Val Lys Ser Gln  
1625 1630 1635  
Arg Glu Gln Ile Glu Glu Leu Gln Arg Gln Lys Glu His Leu Thr  
1640 1645 1650  
Gln Asp Leu Glu Arg Arg Asp Gln Glu Leu Met Leu Gln Lys Glu  
1655 1660 1665  
Arg Ile Gln Val Leu Glu Asp Gln Arg Thr Arg Gln Thr Lys Ile  
1670 1675 1680  
Leu Glu Glu Asp Leu Glu Gln Ile Lys Leu Ser Leu Arg Glu Arg  
1685 1690 1695  
Gly Arg Glu Leu Thr Thr Gln Arg Gln Leu Met Gln Glu Arg Ala  
1700 1705 1710  
Glu Glu Gly Lys Gly Pro Ser Lys Ala Gln Arg Gly Ser Leu Glu  
1715 1720 1725  
His Met Lys Leu Ile Leu Arg Asp Lys Glu Lys Glu Val Glu Cys  
1730 1735 1740  
Gln Gln Glu His Ile His Glu Leu Gln Glu Leu Lys Asp Gln Leu  
1745 1750 1755  
Glu Gln Gln Leu Gln Gly Leu His Arg Lys Val Gly Glu Thr Ser  
1760 1765 1770  
Leu Leu Leu Ser Gln Arg Glu Gln Glu Ile Val Val Leu Gln Gln  
1775 1780 1785  
Gln Leu Gln Glu Ala Arg Glu Gln Gly Glu Leu Lys Glu Gln Ser  
1790 1795 1800  
Leu Gln Ser Gln Leu Asp Glu Ala Gln Arg Ala Leu Ala Gln Arg  
1805 1810 1815  
Asp Gln Glu Leu Glu Ala Leu Gln Glu Gln Gln Ala Gln  
1820 1825 1830  
Gly Gln Glu Glu Arg Val Lys Glu Lys Ala Asp Ala Leu Gln Gly  
1835 1840 1845  
Ala Leu Glu Gln Ala His Met Thr Leu Lys Glu Arg His Gly Glu  
1850 1855 1860  
Leu Gln Asp His Lys Glu Gln Ala Arg Arg Leu Glu Glu Leu  
1865 1870 1875  
Ala Val Glu Gly Arg Arg Val Gln Ala Leu Glu Glu Val Leu Gly  
1880 1885 1890  
Asp Leu Arg Ala Glu Ser Arg Glu Gln Glu Lys Ala Leu Leu Ala  
1895 1900 1905  
Leu Gln Gln Gln Cys Ala Glu Gln Ala Gln Glu His Glu Val Glu

1910	1915	1920
Thr Arg Ala Leu Gln Asp Ser Trp Leu Gln Ala Gln Ala Val Leu		
1925	1930	1935
Lys Glu Arg Asp Gln Glu Leu Glu Ala Leu Arg Ala Glu Ser Gln		
1940	1945	1950
Ser Ser Arg His Gln Glu Glu Ala Ala Arg Ala Arg Ala Glu Ala		
1955	1960	1965
Leu Gln Glu Ala Leu Gly Lys Ala His Ala Ala Leu Gln Gly Lys		
1970	1975	1980
Glu Gln His Leu Leu Glu Gln Ala Glu Leu Ser Arg Ser Leu Glu		
1985	1990	1995
Ala Ser Thr Ala Thr Leu Gln Ala Ser Leu Asp Ala Cys Gln Ala		
2000	2005	2010
His Ser Arg Gln Leu Glu Glu Ala Leu Arg Ile Gln Glu Gly Glu		
2015	2020	2025
Ile Gln Asp Gln Asp Leu Arg Tyr Gln Glu Asp Val Gln Gln Leu		
2030	2035	2040
Gln Gln Ala Leu Ala Gln Arg Asp Glu Glu Leu Arg His Gln Gln		
2045	2050	2055
Glu Arg Glu Gln Leu Leu Glu Lys Ser Leu Ala Gln Arg Val Gln		
2060	2065	2070
Glu Asn Met Ile Gln Glu Lys Gln Asn Leu Gly Gln Glu Arg Glu		
2075	2080	2085
Glu Glu Glu Ile Arg Gly Leu His Gln Ser Val Arg Glu Leu Gln		
2090	2095	2100
Leu Thr Leu Ala Gln Lys Glu Gln Glu Ile Leu Glu Leu Arg Glu		
2105	2110	2115
Thr Gln Gln Arg Asn Asn Leu Glu Ala Leu Pro His Ser His Lys		
2120	2125	2130
Thr Ser Pro Met Glu Glu Gln Ser Leu Lys Leu Asp Ser Leu Glu		
2135	2140	2145
Pro Arg Leu Gln Arg Glu Leu Glu Arg Leu Gln Ala Ala Leu Arg		
2150	2155	2160
Gln Thr Glu Ala Arg Glu Ile Glu Trp Arg Glu Lys Ala Gln Asp		
2165	2170	2175
Leu Ala Leu Ser Leu Ala Gln Thr Lys Ala Ser Val Ser Ser Leu		
2180	2185	2190
Gln Glu Val Ala Met Phe Leu Gln Ala Ser Val Leu Glu Arg Asp		
2195	2200	2205
Ser Glu Gln Gln Arg Leu Gln Asp Glu Leu Glu Leu Thr Arg Arg		
2210	2215	2220
Ala Leu Glu Lys Glu Arg Leu His Ser Pro Gly Ala Thr Ser Thr		
2225	2230	2235
Ala Glu Leu Gly Ser Arg Gly Glu Gln Gly Val Gln Leu Gly Glu		
2240	2245	2250
Val Ser Gly Val Glu Ala Glu Pro Ser Pro Asp Gly Met Glu Lys		
2255	2260	2265
Gln Ser Trp Arg Gln Arg Leu Glu His Leu Gln Gln Ala Val Ala		
2270	2275	2280
Arg Leu Glu Ile Asp Arg Ser Arg Leu Gln Arg His Asn Val Gln		
2285	2290	2295
Leu Arg Ser Thr Leu Glu Gln Val Glu Arg Glu Arg Arg Lys Leu		
2300	2305	2310
Lys Arg Glu Ala Met Arg Ala Ala Gln Ala Gly Ser Leu Glu Ile		
2315	2320	2325
Ser Lys Ala Thr Ala Ser Ser Pro Thr Gln Gln Asp Gly Arg Gly		
2330	2335	2340
Gln Lys Asn Ser Asp Ala Lys Cys Val Ala Glu Leu Gln Lys Glu		
2345	2350	2355
Val Val Leu Leu Gln Ala Gln Leu Thr Leu Glu Arg Lys Gln Lys		
2360	2365	2370
Gln Asp Tyr Ile Thr Arg Ser Ala Gln Thr Ser Arg Glu Leu Ala		
2375	2380	2385
Gly Leu His His Ser Leu Ser His Ser Leu Leu Ala Val Ala Gln		
2390	2395	2400

Ala Pro Glu Ala Thr Val Leu Glu Ala Glu Thr Arg Arg	Leu Asp	
2405	2410	2415
Glu Ser Leu Thr Gln Ser Leu Thr Ser Pro Gly Pro Val	Leu Leu	
2420	2425	2430
His Pro Ser Pro Ser Thr Thr Gln Ala Ala Ser Arg		
2435	2440	

<210> 8  
<211> 153  
<212> PRT  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> Incyte Clone No: 2195418

<400> 8  
Met Ala Arg Asn Thr Leu Ser Ser Arg Phe Arg Arg Val Asp Ile  
1 5 10 15  
Asp Glu Phe Asp Glu Asn Lys Phe Val Asp Glu Gln Glu Glu Ala  
20 25 30  
Ala Ala Ala Ala Ala Glu Pro Gly Pro Asp Pro Ser Glu Val Asp  
35 40 45  
Gly Leu Leu Arg Gln Gly Asp Met Leu Arg Ala Phe His Ala Ala  
50 55 60  
Leu Arg Asn Ser Pro Val Asn Thr Lys Asn Gln Ala Val Lys Glu  
65 70 75  
Arg Ala Gln Gly Val Val Leu Lys Val Leu Thr Asn Phe Lys Ser  
80 85 90  
Ser Glu Ile Glu Gln Ala Val Gln Ser Leu Asp Arg Asn Gly Val  
95 100 105  
Asp Leu Leu Met Lys Tyr Ile Tyr Lys Gly Phe Glu Lys Pro Thr  
110 115 120  
Glu Asn Ser Ser Ala Val Leu Leu Gln Trp His Glu Lys Ala Leu  
125 130 135  
Ala Val Gly Gly Leu Gly Ser Ile Ile Arg Val Leu Thr Ala Arg  
140 145 150  
Lys Thr Val

<210> 9  
<211> 1185  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> Incyte Clone No: 1274060

<400> 9  
cacagccaca gcccctgact gcccgcagccc ccacagagcc cggccgcgcac cccacgtccc 60  
ccacgcccagc gcccagccat ggaggccatc aagaagaaaa tgcagatgct gaagttggac 120  
aaggagaatg ccatcgaccc cgcggagcag gcgaggccgg ataagaaagc cgctgaggac 180  
aagtgcagaagc aggtggagga ggagctgacg cacctccaga agaaaactaaa agggacagag 240  
gacgagctgg ataaatattc cgaggacctg aaggacgcgc aggagaagct ggagctcacg 300  
gagaagaagg cctccgcacgc tgaaggtgat gtggccgccc tcaaccgacg catccagctc 360  
gttgaggagg agttggacag ggctcaggaa cgactggcca cggccctgca gaagctggag 420  
gaggcagaaa aagctgcaga tgagagttag agaggaatga aggtgataga aaaccgggcc 480  
atgaaggatg aggagaagat ggagattcag gagatgcacg tcaaagaggc caagcacatt 540  
cgccgaagagg ctgaccgcaa atacgaggag gtatcgta agctggcat cctggagggt 600

gagctggaga gggcagagga gcgtgcggag gtgtctgaac taaaatgtgg tgacctggaa 660  
 gaagaactca agaatgttac taacaatctg aatctctgg aggctgcattc tgaaaagtat 720  
 tctgaaaagg aggacaaata tgaagaagaa attaaacttc tgcgtgacaa actgaaagag 780  
 gctgagaccc gtgctgaatt tgcagagaga acgggtgcaa aactggaaaa gacaatttat 840  
 gacctggaaag agaaaacttgc ccaggccaaa gaagagaacg tggggttaca tcagacactg 900  
 gatcagacac taaacgaact taactgtata taagcaaaac agaagagtct ttgttcaaca 960  
 gaaactctgg agtccgtgg gtctttctt tcttgcataa gaagttcctt ttgttattgc 1020  
 catcttcgct ttgctggaaa tgtcaagcaa attatgaata catgacccaa tattttgtat 1080  
 cgggagaagct ttgagcacca tggtaatct cattccttc ctttttttt caaaaaaaaaa 1140  
 aagagatagg attgagtggg aggaaaaaaa aaaaaa 1185

<210> 10  
 <211> 1050  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte Clone No: 1577078

<400> 10  
 gttttttccca gacattttcc gggaaatca tactgaaatt ttggatgag tggaaattcc 60  
 ctatggctg gactcctggg tgggcttga cagggaaat caggttaaca gagggcagga 120  
 catgggggg gctccactg gtggctggcc tgatacttct taacatggct gcaccccgaa 180  
 cctcccccagg ctgaagggtga tggggccgccc ctcaaccgac gcatccagct cgttggggag 240  
 gagttggaca gggctcagga acgactggcc acggccctgc agaagctgga ggaggcagaa 300  
 aaagctgcag atgagagtga gagagaaatg aaggtgatag aaaaccgggc catgaaggat 360  
 gaggagaaga tgagagattca ggagatgcag ctcaagaggc ccaagcacat tgcggaaagag 420  
 gctgaccgca aatacggaga ggtagctcg aagctggta tcctggaggg tgagctggag 480  
 agggcagagg agcgtgcggg ggtgtctgaa ctaaaatgtg gtgacctgga agaagaactc 540  
 aagaatgtt ctaacaatct gaaatctctg gaggctgcat ctgaaaagta ttctgaaaag 600  
 gaggacaaat atgaaagaaga aattaaactt ctgtctgaca aactgaaaga ggctgagacc 660  
 cgtgctgaat ttgcagagag aacggttgc aactggaaa agacaattga tgacctggaa 720  
 gagaaacttg cccaggccaa agaagagaac gtgggcttac atcagacact ggatcagaca 780  
 ctaaacgaaac ttaactgtat ataagaaaaa cagaagagtc ttgttccaaac agaaactctg 840  
 gagctccgtg ggtctttctt ttcttgcataa gaagttctt ttgttatttgc ccatcttcgc 900  
 ttgctggaa atgtcaagca aattatgaat acatgacccaa atattttgttgc tggagaagc 960  
 tttgagcacca atgtttaatc tcattccttc ctttttttt tcaaaaaaaaaa aaagagatag 1020  
 gattgagtgg aagggttaggg gaggaaaaaaa 1050

<210> 11  
 <211> 729  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte Clone No: 1426711

<400> 11  
 cgctccctccg cccgaccgcg cgctcgcccc gcccgtcctg ctgcagcccc agggccctc 60  
 gcccggcca ccatggacgc catcaagaag aagatgcaga tgctgaagct cgacaaggag 120  
 aacgccttgg atcgagctga gcaggcggag gcccacaaga aggccggcga agacaggagc 180  
 aagcagctcg aggaggacat cgccggccaag gagaagggtgc tgcgggtgtc ggaggacag 240  
 cgggaccggg tgctggagga gctgcacaag gcccgggaca gcctcctggc cgccgaagag 300  
 gcccggcca aggtgtaagc cgacgttagct tctctgaaca gacgcatcca gctgggttag 360  
 gaagagttgg atcggtccca ggagcgtctg gcaacagctt tgcaagact ggaggaagct 420  
 gagaaggcag cagatgagag tgagagaggc atgaaatgtca ttgagagtc agccaaaaaa 480  
 gatgaagaaaa aatggaaaat tcaggagatc caactgaaag aggccaaagca cattgtctaa 540  
 gatccgacc gcaaatatga agaggtggcc cgtaaagcttgc tcattcattga gagcgactg 600  
 gacgtgcag aggacgggc tggagaaggc ctggataaaag acagaaggc ggcaacacac 660

caccccccagcc cccaccccca cccttcctt gagttctgt gaattaaaat atttgc当地 720  
ccaaaaaaaaa 729

<210> 12  
<211> 2068  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> Incyte Clone No: 1676756

<400> 12  
gcagccagaa ccgagtcagc cataaagcta cgcgcctaggc tcttggccct gacgtgaggg 60  
gcccagagat ggcgttaacgg gaatagttt caacgtctat ttcatccct gcttcagagg 120  
acctctttaa tctttgatt tggccctgt ttctaaagaaa agcaactgaa aaggctgtaa 180  
taccggccct gagaaaaaaag gagcagcgct aaataatcga gaaaatgcct cctcttggaa 240  
cgatataaga gatggaaaca agatataaga aggattgaga atcatataat acaggagctt 300  
aaacacccat ggcgtatgt aaagaggta ctattagagc gcttggaaaa taccaggaag 360  
tttagagagt taacagaagg ggcgcacgtg gattggccac aaaatcgaat tactgaagta 420  
agtcaaaac gacaaattgt cacagaatac agagaaaaagg gggaaaagaaa ttacgaggag 480  
aaaaagagag atcttagaggc cgggtccagg agataacaat tatgcataat aggaataacct 540  
gaaactgaggc acagagcaag tggagctgaa acaaataaagg atctacttga aaaaaatttt 600  
ccagaattga agaaacgaact agatctacaa atggaaaagg ctcataggat acctttaaag 660  
tttaatgaaa agaaagcgc atctagacat atccgggtga cgttttgaa ttccaaagac 720  
gaaacatttt acaagcatcc agtcagagaa agcagggtac ttacaaagg gcaaaagtca 780  
ggctgacctc agattttct cctgcattt taaatgccag aagacagtgg aacaataatct 840  
agagtgttaa gggaaaataa ttttgcattt agaattatat actctgccaa gttatcattt 900  
ctttacaaag gaaactggaa gacattctt gatatacagg gtttaggaaa gtatataac 960  
caagaacttt ccctgaaaat tttgtgttgc gatttactgc agtcaacaga gAACCTGAAT 1020  
taaaataaga atagggaggc aattgtatga aagaactgtat ggtatgcatt aaaaactgtt 1080  
aaggagcatt aagttaaat ttttgcattt agggcattaa aactaaatac aaaaatagaa 1140  
acataagctg ggtgtaaaat ttcgtttac gttttaactg gaagggcata ccacatgttc 1200  
aatatattgg acaaataactg ttttgcattt agcatgtatg attgtatgaa caaatacgc 1260  
tggcgtttaaag ctaaacctaa gtaaaaggc tttgtactg tagatttgac aaataacatt 1320  
ctaaatgtca aatctgacaa ttggaaaaca gtacagttt atttccctt ttttaagta 1380  
tagcaggaaa aaaataacaa gtttgtccat gttactactg atactgtaaa gaaacttcca 1440  
aatcactgg tttggggggg gtggatacat cctcattttc tgtacatgat gcatggggaa 1500  
aaacagtagt tactgcatca tatagttcca agttaatcat atagttccaa gtaaatttga 1560  
catggaaaata agtgttaact aaaaaatag aatataataca ttccaatgtt tggaaaagaa 1620  
gtggtaaaaaa gaaaaataagc aaaaagacac taaaatttagc aaaaagttaga ttgacagtac 1680  
agatgaccta taaactgggtt aaatagccct attacaattt aattgggtc aaaaatcaat 1740  
ctctaaccctg agatacattt gtataaaaca aatgtatcaa gagtttaaag ataatggaaa 1800  
ctataaatca tagaaatagc aacattttt taaaatcta aacataagac attttatgtt 1860  
aaacatacaa tataggatgt aacatttaac aaactatatg gtaaaaataa tgacattaaat 1920  
atataaaata tatgttccag atctgtatgt ggggtatgt tttactatg tacatcgata 1980  
tacatctatt taaaacatg tacattttaa ttgttgcatt ttatgtatgtt aaaaattttt 2040  
gagtaatcct tctgtatgtt ttatataat 2068

<210> 13  
<211> 3191  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<223> Incyte Clone No: 1843770

<400> 13  
aggcaggcaa aaggaggatcat ggcttctgtat gcttagtcatg cgctggaaagc tgccctggag 60  
caaatggacg ggatcatttc aggactaaa acaggtgcag atcttagtga tggtaatgtt 120  
gagcctggac tggcttcccc ggcctcctac atgaaccctt tcccggtgtt ccatctcatc 180

gaggacttga ggctggcctt ggagatgctg gagcttcctc aggagagagc agccctcctg 240  
 agccagatcc ctggccaaac agctgcctac ataaaaggaat ggttgaaga gagcttgc 300  
 caggtaaacc accacagtgc tgcttagtaat gaaacctacc aggaacgctt ggcacgtcta 360  
 gaaggggata aggagtcct catattgcag gtgagtgtcc tcacagacca agtagaagcc 420  
 cagggagaaa agattcgaga ccttggaaatg tgcgttggaa gacaccaggtaaaactcaat 480  
 gctgctgaag agatgcttca acaggagctg ctaagccgca catctcttga gacccagaag 540  
 ctcgatctga tgactgaagt gtctgagctg aagctcaagc tggttggcat ggagaaggag 600  
 cagagagagc aggaggagaa gcagagaaaaa gcaagaggat tactgcaaga gtcaggcac 660  
 ctcaaaatca aagtggaaatg gaaaggaaatg agtataatg gaagctaaatg 720  
 gccactaagg ctgaagtgc ccaactgcaaa gacacagggtt cccttggaaatg tgcagaaatt 780  
 gagcgtctgc acaggcagct cttccggaca gcagctctcc acagtggagatc tccacacagag 840  
 agagacaaatg aaatccaaatg tcttggaaatg gggatggaaa ctttgcgtct tgccaaatgaa 900  
 gataaggacc gtcggataga ggagcttacg gggctgttac accagtaccg gaaggtaaaag 960  
 gagattgtga tggtactca agggcttgc gagaacttctc tctcaatcaa tgaagaagaa 1020  
 ccggagggag gtttgcgttca gtttgcgttca acaaataagg acccttgcgttca attatggaa 1080  
 caagagatgc ctccaaatg tagctcttcc acagtggggc caccccttgcgttca gccacagaaa 1140  
 tcactggaaa ccaggcgtca gaaaaagctc tcttgcgttca tagaagactt gagaagtggaa 1200  
 tcttgcgttca agtgcgttca tgggaaaccag cccttcccg tggatggaaatg caaggacagc 1260  
 ctttgcgttca cggagcacaatg atatccactt tttgcgttca agtgcgttca agccacgccc 1320  
 aatggagggatg ctgccaatgc tccctccacc atctggccagc ctgacccac gggggagcagc 1380  
 ctgctgagggatg tgagagacac agaaatggc tggatggaca ctgctgttgcgttcaatgaccc 1440  
 tcatccacat catcggcgtca tgaatcaggat cttcgttca tcttgcgttca agatggtaaa 1500  
 cggaaatccaa aaggccatggaaatg gggatggggatg gaaagaactca gtcagggaaatg 1560  
 ttcttgcgttca acacgcttgg gatggcagatc tttcgttca gtttgcgttca ggcacccgc 1620  
 gggccaaatgc tcttgcgttca caggcgttca aaggccatggaaatg gggatggggatg 1680  
 ttttgcgttca gggatggggatg gggatggggatg gggatggggatg gggatggggatg 1740  
 tatgtatct ttgcgttca gtttgcgttca tcttgcgttca ctttgcgttca agccacccct 1800  
 caggacatgg aaaaaggagct aggaatggaaatg cacccttgcgttca acaggaaatg gtttgcgttca 1860  
 gcagtggaaatg ccatcaacac caaacaggag gggatggggatg gggatggggatg 1920  
 gtgacaatggatg ggcttgcgttca tatttgcgttca ccccttgcgttca aagaccatggatg 1980  
 agatggatggatg gacggatggatg gcaatggggatg acttgcgttca atttgcgttca 2040  
 accagccaaatg tacatcatct ctttgcgttca gggatggggatg gggatggggatg 2100  
 ttcaacccccc acttgcgttca cccggccggcc gtttgcgttca gtttgcgttca gtttgcgttca 2160  
 gtttgcgttca gggatggggatg gggatggggatg gggatggggatg gggatggggatg 2220  
 tatgcacccca atcttgcgttca gggatggggatg gggatggggatg gggatggggatg 2280  
 ttttgcgttca gggatggggatg gggatggggatg gggatggggatg gggatggggatg 2340  
 cggccacccca ccccaatggatg ctttgcgttca gggatggggatg gggatggggatg 2400  
 gagaaaatggatg ctttgcgttca gggatggggatg gggatggggatg gggatggggatg 2460  
 aaacttaggat ttttgcgttca gggatggggatg gggatggggatg gggatggggatg 2520  
 tacatttgcgttca ctttgcgttca gggatggggatg gggatggggatg gggatggggatg 2580  
 taccggggcc ttttgcgttca gggatggggatg gggatggggatg gggatggggatg 2640  
 attatgtatct ttttgcgttca gggatggggatg gggatggggatg gggatggggatg 2700  
 gtgtgttgcgttca atataacttgc accttgcgttca gggatggggatg gggatggggatg 2760  
 ccagcaatttgcgttca gggatggggatg gggatggggatg gggatggggatg 2820  
 gtttgcgttca taaggggccatggatg gggatggggatg gggatggggatg 2880  
 gacactttaatg gacacttgcgttca gggatggggatg gggatggggatg gggatggggatg 2940  
 gaaacacatg aacttgcgttca gggatggggatg gggatggggatg gggatggggatg 3000  
 tcaggccatggatg ctttgcgttca gggatggggatg gggatggggatg gggatggggatg 3060  
 ctttgcgttca gggatggggatg gggatggggatg gggatggggatg gggatggggatg 3120  
 ttgtgttgcgttca gggatggggatg gggatggggatg gggatggggatg gggatggggatg 3180  
 gggaaatggatg 3191

<210> 14  
 <211> 3164  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte Clone No: 3768043

<400> 14  
 aggtttaatc catgaagaatg acagcaatggatg taaaatggatg ttcacccaaaa aataaaatggatg 60  
 caaaaatggatg gatgtggaaaatg ctggccagaac taaggccggcc cgggctcaga ccagcgctgc 120

ctcaggatgt aaagtgtAAC aagaggGCCa gggaggtgg tggggacAA catgggcTG 180  
 tgaggcCTgt gggTgCCCGC gttccccAGC tccccccGCA gcccGCTCCA cAGTGGTCCG 240  
 ctccggTTgg ttgtcacGTg cgcattcGGG ttccAGACCC aaggCTGCGT gttCTCCACC 300  
 gcttggTTgt gccAGTgtTA ctgCGGTGAC CGCCAGAGCA gcCTGACGC tatggaggAG 360  
 cctggTgCTA cccCTCAGCC ctacCTGGG ctggTCTGG aggAGCTACG cAGAGTGTG 420  
 gcAGcACTAC ctgAGAGTAT gagACCAgAT gagaATCCTt atggTTTCC atCGGAACtG 480  
 gtggTATgtg cAGCTGTTat tggATTTTt gttGTTCTCC ttttttGt gagaAGTTT 540  
 agatCGGTtA ggAGTCGGt ttacGTGGGA agAGAGCAAA aacttGtGtC aacGCTTtC 600  
 ggactaATTg aagaaaaATtA taaACTACTt gaaaaATTtA gcCTTATTCA aaaAGAGTAT 660  
 gaaggCTATg aagtAGAGTC atCTTtAGAG gatGCCAGt ttGAGAGGA ggcAGCAGAA 720  
 gaAGCAGCAGAA gttGGAGGc aacCTGTgAA aAGCTGAACA ggtCCAAATTc tGAACtTGAG 780  
 gatgAAATCC tCTGTCTAGA aaaAGACTTA AAACAAGAGA aATCTAAACA ttCTCAACAA 840  
 gatgAAATTgA tGGCGGATAT ttCAAAAAGT atACAGTCTC tagAGATgA gTCAAAATCC 900  
 ctCAAAATCAC AAATAGCTgA agCCAAATC atCTGCAAGA cATTAAAT gAGTGAAGAA 960  
 cgACGGGCTA tagCAATAAA agATGTTTg aATGAAATT CTCAACTTCa gACAAGCCAT 1020  
 aaACAGCTTt tTCAGCAAGA agCTGAAGTA tggAAAGGAG aAGTGAAGTgA actTAATAAA 1080  
 cAGAAAATAA cATTGAAAGA CTCCAAAGTA cACGcAGAAc aAGTTCTGAA tgATAAAGAA 1140  
 aATCACATCA agACCCtGAC tggACACTTg cCAATGATgA aAGATCAGGc tGCTGTGCTT 1200  
 gaAGAAgACA caACGGATgA tgATAACCTG gaATTAGAAG tGAACAGTgA atCGGAAAT 1260  
 ggtGCTTACT tagATAATCC tCCAAAAGGA gCTTGTGAAAG aACTGATTCA tGCTGTCAAG 1320  
 tTAATGCTT cTTAAAAC cTTAGAGGA gAAAGAAACC AAATTATAT tCAGTTGtC 1380  
 gaAGTGTATA AAACAAAGAGA agAGCTTACa gAGCATATTA AAAATCTTCa gACTCAACAA 1440  
 gCATCTTGC agTCAGAGAAAC cACACATTtTt gAAATGAGA atCAGAAGCT tCAACAGAA 1500  
 ctTAAGATAA tgACTGATTtTt atATCAAGAA aATGAAATgA aACTCCACAG gAAATTAAACA 1560  
 gtagAGGAAA ATTATCGGTt agAGAAAGAA gAGAAACTTt cTAAGTgA tgAAAAGATC 1620  
 agCCATGCCA CTGAAGAGCT ggAGACCTAT AGAAAGCAG gCCAAAGATCT tGAAGAAGAA 1680  
 ttGGAGAGAA CTATTCTTc ttATCAAGGG CAGATTATTtTt cCCATGAGAA AAAAGCACAT 1740  
 gataATTGGT tGGCAGCTG gaATGCTgAA agAAACCTCA atGATTtAAG gAAAGAAAAT 1800  
 gCTCACAACA gACAAAATTt aACTGAAACA gAGCTTAAT tTGAACTTTTt AGAAAAGAGt 1860  
 cCTTATGcAC tCGATGTTCC AAATACAGCA tttGGCAGAG AGCATTCCCC ATATGGTCCC 1920  
 tcACCATtGG gTGGCCTTC ATCTGAAACA AGAGCTTTc tCTCTCCTCC aACTTGTGt 1980  
 gAGGGTCCAC tCAGACTCTC acCTTGTCTT CCAGGGGGAG gAGGAAGAGG CTcACGAGGc 2040  
 ccAGGGAAcT CTCTGGACCA tCAGATTACc aATGAAAGAG gAGAATCAAG CTGTGATAGG 2100  
 ttaACCGATC CTCTAGGGC tCCCTCTGAC ATGGGTCTC tGTCACCTCC atGGGACCG 2160  
 gACCGTAGGA tGATGTTCC tCCGGCAGGA CAATCATATC CTGATTCTAGC CTTCTCTCA 2220  
 cAAAGGCAAG ACAGATTtTt ttCTTAATTCT gGTAGACTGT CTGGACCGAG AGAACTCAGA 2280  
 agTTTAATA tGCCTTCTTT ggATAAAATg gATGGGTCAA tGCCTTCAgA AATGGAATCC 2340  
 agTAGAAATG ATACCAAAAGA tGATCTGGT AATTAAATG tGCCTGATTc ATCTCTCCt 2400  
 gCTGAAATG AAAGCCACTGG CCCTGGCTTt gTCCCTCCAC CTCTGTCTC AATCAGAGGT 2460  
 ccATTGTTc CAGTGGATGC AAGAGGCCA tTCTTgAGAA gAGGACCTCC tttCCCCCA 2520  
 cCTCCTCCAG gAGCCATGTT tGGAGCTCTC CGAGATTATTtTt tTCCACCAAG ggATTTCCCA 2580  
 ggtCCACCAc CTGCTCCATT tGCAATGAGA aATGTCTATC CACCGAGGGG tTTCTCTCCt 2640  
 tacCTTCCCC CAAGACCTGG ATTtTCCCTC CCACCCCCAC ATTCTGAAGG TAGAAGTgAG 2700  
 ttCCCTCTAG gTTGATTCC ACCTTCAAT gAGCCTGCTA CTGAACATCC AGAACCCACAG 2760  
 caAGAAACtTt gACAATTTCTT cAAAGTAAT tTtGACTGAT CTcATTtTCA 2820  
 gTTTAAGTAA CTGCTGTTAC tTAAGTgATT ACACTTTGtC tCAAATTGAA gCTTAATGGA 2880  
 attATAATTtC tCAGGATAGT ATTtTGTAAAG tAAAGATGAT tAAATATgA ATCTTATGAG 2940  
 tAAATTATTtC tAAATTtATTtC tTAGACGGTA TAActATTtC AATTGATTA ATCCACTATT 3000  
 atATAAAACAA tagTGGGAGT tttATATATG tAAATCTTCa gGTGGGGAGG CTtAAATTc 3060  
 tGAAGTCTGT gTCTTATGC CAAGAACTGT ATTACTGTG gTTGAGACa AATGTGAAG 3120  
 TAActTTATG CTtAAATAAA ttATAGTgA tttAAAtAAA AAAA 3164

<210> 15  
 <211> 7962  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <223> Incyte Clone No: 1655208

<400> 15  
 aaaAGTAGGA AGGTAGAGTT gttGGCAGAA ATCCtGGGAT aAGAGAATAG tttCCTGAA 60  
 gATCTGTGcC tCCAAcCCAGC AGAGAGGGAT tGAGCTTCAAC AGAGCCAAcA 120

tttcatacgca ccatgttcaa gaggaggtt aagtggcatg gcaatggta gagaccctgc 180  
tgggcgtgaa caccctctgg ctaccttaggg acctgtggc ctaccacccg gtgcctcat 240  
ggagacaaga agccctgggt tgaacaacat gaagccccag tcactgcgc tggtactgga 300  
agagcagggtg ctggcactac agcagcagat ggcagagaat caggcagcct cctggcgaa 360  
gctgaagaac tcccaggagg cccagcagag acaagcaacc cttgtgagga agtgcaggc 420  
caaggtgctg cagtaccgaa gctgggcca agagctggag aagcggctag aagccactgg 480  
aggaccaatc cccagaggtt gggaaaatgt ggaggagcc aacctggat agtgcgtgg 540  
ccgatggag gaggagcaac agaggtgtga gactctagca gaggtaaaca cccagatcc 600  
actgcacatc gaaaaagctg acgtggtaa taaggccctt agggcagat tgaaaaaaact 660  
gacagtggac tggagccggg cccggatgaa gctaattgagg aaggagagcc agtggcagat 720  
ggagcaggag ttcttcaagg gctacctgaa agggagcac ggtgccttc tcagtcata 780  
gcgggagggtt gtgacattcc gacgcaactt cctggaaatg aagtcaagta ctgacagaga 840  
tctgtatggag ctaaaagctg agcatgtgag gctttcaggg tctctgttga cctgttgc 900  
gcgcttact gttggagcac agtctcgga acccaacggg tctggaaagaa tggatgggc 960  
ggagccggcc cagctgctg tgctactagc caagacccag gagctggaga aggaagccca 1020  
tgaaggagc caggagttaa tacagctgaa gactcaaggg gatctggaga aggctgaact 1080  
tcaggaccgg gtgaccgagc tctctgttct gtgaccctg tctcagaagc aaaatgaaga 1140  
ttatgaaaag atgataaaagg ctctgagaga gacagtggag atcctggaga caaatcacac 1200  
agaattaatg gaacatgaag catctcttag taggaatgcg caagaggaga agttgtctt 1260  
acagcagggtg atcaaggata taaccaggat catggtggaa gaaggggaca atatagccca 1320  
aggctctgtt ctgtgagaact ctttggatt ggagtctagt atcttctcc agttgttata 1380  
ccaagatgca gacaaggctc ttactctggt gcttctggat ctgactcgga gacgcccggc 1440  
tgtcaggagc ctaaggcagc agcttcagg ctgtcaagag gctgtaaact tggtcaaca 1500  
gcagcatgtat cagtggagg aagagggca agccttgaga cagcggctgc agaagctcac 1560  
tggggagcgg gacactctgg cagggcagac tttggacccctc cagggagagg tggactctc 1620  
cagcaaggag cgagagctgc tgcagaaggc cagggagagg ctgcggcagc agctggaggt 1680  
gctagagcag gaggcatggc gcctgcgaag gttaaatgtg gagcttcagc tgcaaggggg 1740  
ctctgcccag gcccagaagg aggaacagca ggaggagctg cacctggctg tccggagag 1800  
ggagcgtctt caggagatgc tgatggcct ggaagccaaa cagtcaaat cactcagtga 1860  
actgatact cticgggaag ccctggagtc aattcacctg gaagggaggt tactgaggca 1920  
agagcaaacg gaagtgaccg cagcgctggc tagggcagag cagtcaattt cagagctgc 1980  
gagttctgaa aacaccctga agacagaatg agctgtatct cgggtcgcag ctgtcaagat 2040  
cagtgccttta aatgaggctt tggcgttaga taaagggtggg ctgaaccaggc agttctcca 2100  
gttagaggag gagaaggact ctgtgtcag cagaatggag gccgcagagc aggcagaaaa 2160  
tgctgtcag gtcgacctgg cggaggcaga gaagaggagg gaagccctgt gggaaaagaaa 2220  
caetcacctg gaggctcagc tgcagaaaagc tgaggaggctt gggctgagc tgcaaggcaga 2280  
tctcaggagc atccaagaag agaaggaaaga aattcaaaaag aaactaagtg agtcacgtca 2340  
ccagcaggag gcagccacga ctcagctgg cagactacat cagggaggca agcgcacagga 2400  
agaagtctt gccaggggcag tccaggagaa ggaggcccta gtacgagaga aagcggctct 2460  
agagggtcgg ctgcaggccg tggagcgtga cccggcaggac ctgcgtcaca aactacagg 2520  
gctcagctca gccaaggagc tactggagag cagtcgttta gaagccaaac aacaaaattc 2580  
tgtgatagac gagccgcagg ggcagctgg ggtccagatt caaactgtca ctcaagccaa 2640  
ggaagtaatc caaggggaag tgaggtgcct gaagctggaa ctggacactg aacggagtc 2700  
ggcagagcag gacggggatg ctgcagccag acagctggcc caggctgagc aagaaggggaa 2760  
gactgcctt gaggcagcaga aggccagccca tgagaaagag gtgaaccaggc tccggagggaa 2820  
atgggagaag gagegtctct ggcaccaggc ggagctggca aaggctctgg agagctttaga 2880  
aaggggaaaaa atggagctgg aatagggtt aaggagcagc gagacagaaa tggaggccat 2940  
ccaggcccg agggagaag aacggaccca ggcagagat gccctatgcc agatgcagct 3000  
ggaaacagag aaggagagag tatccctctt ggagacactg ctgcagacgc agaaggagct 3060  
agcagatgcc agccaacaac tggAACGACT gaggcaggac atgaaagtcc agaaattaaa 3120  
ggagcaggag accactggga tactacagac ccagctccag gaggctcaac gggagctgaa 3180  
ggaggcagcc cggcagcaca gagatgaccc tgctgcctc caagaagaga gcagctccct 3240  
gctgcaggat aagatggacc tgcagaagca ggtggaggac ttgaagtctc agctgggtgc 3300  
ccaggatgac tcccagaggc tggtggagca ggaggttcag gagaagctga gagagaccca 3360  
ggagtataac cgaattcaga aggagctgg gagagagaaa gccagctga ctctgtact 3420  
gatggaaaag gaacagagac tcctgtttt acaagaagct gacttattt gacaacaaga 3480  
gctgagtggcc ctgcggccagg acatgcagga gcccaggaa gaacagaaa agtgcagtgc 3540  
tcagatggaa ttactaaggc aagaggtgaa gaaaaggag gctgtactt tggcccgagg 3600  
agcacacgt ctggaggagc tggaggcgtc tcatatcagc gaggcagcgc tgcgagccctc 3660  
cttggggcc caggaaggca aggccggca actacacctg cagactgcgc gcacagagag 3720  
ccagctagaa gcgtggcccg cagagcagca gcccggggac caggcccagg cccaggccca 3780  
gctggccagg ctctactctg ccctgcagca gcccctgggg tctgttgc agagcaggcc 3840  
tgagctgagt ggtggggag actctgtcc ttccgtctgg ggccttgagc cagaccagaa 3900  
tggagctagg agcctcttta agagaggcc cctgctgact gctctctccg ctgaggca 3960  
agcatctgcc ctcccaagg ttcataaga cctgtggaa actcaacaga cccggatgt 4020

tctggaggat cagggtccaga aacttggaaaga gcgtctaact gatactgagg ctgagaagag 4080  
ccaggcccac acagagtgc aggatctgca gagacagctc tcccaagaatc aggaagagaa 4140  
atccaagtgg gaaggaaagc agaactccct agaatctgag ctgatggAAC tacatgaaac 4200  
tatggcatcc ttacagagtc gcctgcggag agcagagctc cagcgaatgg aagcccagg 4260  
tgagcgagag ttacttcagg cagccaaagga gaacctgaca gcccagggtgg aacacctgca 4320  
agcagctgca gtagaaagcc gggctcaggc aagtgtctgc ggcattctgg aagaagacct 4380  
gagaacggct cgctcagcac tgaagctgaa aaatgaggaa gtagagagtg agcgtgagag 4440  
agcccaggct ctgcaagagc agggcgaact gaagggtggcc caagggaaagg ctctgcaaa 4500  
gaatttggcc ctctgtaccc agaccctagc tgaagagagaa gaggagggtgg agactctgc 4560  
gggacaatac caggaactgg agaagcaacg gaaatgcag aaggctgtt tggatttgct 4620  
gtctctggac ctgaagaaga ggaaccaaga ggtatctg cagcaagaac agattcagga 4680  
gctagagaag ttaggtctg ttttagagca tctgcccattt gccgtccagg agcgagagca 4740  
gaagctgact gtgcagaggg agcagatcag agagctcgag aaggatcgaa agactcagag 4800  
gaacgtttt gacatcagc ttctagaact tgagaagaaa gaccaatga ttgagtc 4860  
gagaggacag gttcaggacc tgaaaaagca gttggttact ctggaatgcc agctggaggg 4920  
actggaggaa aaccatcaca agatggagtg ccagcaaaaa ctgatcaagg aagaaaggag 4980  
ccagaggaa acccagagag tggcttgc ccaccttacg ctggacctaag 5040  
ccaggagctg cagggcacaag gcagccagat ccatgacctg gagagccaca gcaccgttct 5100  
ggcaagagag ctgcaggaga gggaccagg ggtgaagttt cagcgagaac agatcgagga 5160  
gctgcagagg cagaaagagc atctgactca gatctcgag aggagagacc agggctgtat 5220  
gctgcagaag gagaggattt aggttctcgat gatcgaggg accccggaga ccaagatct 5280  
ggaggaggac ctggaacacaa tcaagctgtc cttggagagg cgaggccggg agtgcacac 5340  
tcagaggcag ctgatgcagg aacggggcaga gaaagggaag gcccagaat aacacagcg 5400  
cggggccta gacatcgatc agctgtatctt gctgtataag gagaaggagg tggatgtca 5460  
gcaggagcat atccatgcac tccagggactt caaagaccag ctggagcagc agctccagg 5520  
cctgcacagg aagtaggtt agaccaggctt cctctgttcc cagcgagagc agggaaatagt 5580  
ggtcctgcag cagcaactgc aggaagccag ggaacaagg gactgtgagg aacactggagg 5640  
tcagagtcac ctggatgagg cccagggactt cctagcccaag agggaccagg aaaaaggcaga 5700  
tctgcagcaa gaacagcagc aggcccaggg acaggaggag agggtgaagg atggagagct 5760  
cgccctccag ggagctctgg agcaagccca tatgacactg aaggagcgtc agggacggcg 5820  
tcaggaccac aaggaacagg cacgaaggct ggaggaagag ctggcagtgg aacaggagaa 5880  
ggtccaggcc ctggaggagg tgctgggaga cctaagggt gactctcg 5940  
agctctgtt gcccctccagc agctgtgtc tgagcaggca caggagcatg aggtggagac 6000  
cagggccctg cagggacactt ggctcgaggcc ccaggcgtt gctcaaggaa gggacccaga 6060  
gctggaaact ctgcgggcaag aaagtctgtc tctccggcat gaggaggagg ctgcccggc 6120  
ccgggtctgag gctctgcagg aggcccttgg caaggctcat gctggccctgc agggaaaga 6180  
gcagcatctc ctgcaggcagg cagaatttgag ccgcgtctg gaggccagca ctgcaaccct 6240  
gcaagccctc ctggatgcctt gccaggcaca cagtcggcag ctggaggagg ctctgaggat 6300  
acaagaaggt gagatccagg accaggatct ccgataccag gaggatgtc aacagctgca 6360  
gcaggcaactt gcccagggg atgaagagct gagacatcag caggaacccggg agcagctgt 6420  
ggagaagtct ctggcccaaga gggtccaaga gaatatgtc caagagaagc agatctgggg 6480  
gcaagagaga gaagaggagg agataagggg ctttcatcag agttaaggg aactacagct 6540  
gactctagcc caaaaggaaac aggagattct ggagctgagg gagaccacaa aaagaaccaa 6600  
cctggaaagcc ttacccacaa gccacaaaatc ctcccaatg gaggaaatc ctctaaaact 6660  
tgattttt gagcccaaggc tgcaaggggc gttggaggcg ctacaggcag ccctgagaca 6720  
gacagaagcc agggagattt agtggaggga gaaggcccg gacttggcac tctccctagc 6780  
gcagaccaag gccagtgtca cagatctgc gaggatgtt atgttcttac aagcttgggg 6840  
cctggaggcg gactcagaac agcaaaagggt gcaatgtc ctggagctca cccaggcagg 6900  
tctggagaag gaggcgttac acagccagg tgcaaccagc acagcagaac tgggtccag 6960  
aggggagcg ggtgtcagg tggagagggt ctcaaggatg gaggctgagc ctgcagcaag 7020  
tggatggag aagcagtcat ggagacaaag gcttgaacac cagctgcggg cagcaggatg 7080  
gctggagatt gacaggagca ggctgcagcg ccacaatgtc cagctgcggg gtaccttgg 7140  
gcaggtggag cgagaacggg ggaagctgaa gaggaggccc atgcgtgcgg cccaggcagg 7200  
gtcccttagag atcagcaagg ccacggctt ttccacccaca cagcaggatg ggagaggaca 7260  
gaagaactca gatgccaatgt gttggctga actgcagaaaa gagggtgtcc tgctgcaga 7320  
tcagctgact ttggagcggg agcagaagca ggactacatc acccgcctcg cacagaccag 7380  
ccgtgagcta gcaggcctgc accacagcct ctcacacta ctcttgcgg tggccaggc 7440  
ccctgaggcc actgtcttgg aggcagagac cccgagggtg gatgagttcc tgcgtcaac 7500  
tctgacatcc ccaggccag tcctgttaca ccccaaggccc agactacacc aagccgcctc 7560  
caggttagcag ccacaggccag gagcacacag agcaaaaggact gtgtcatggg tcatggccc 7620  
tccgcacacc tacagggtt ccaaaggaaa agcctggctc tggtaggcac ccaggagccc 7680  
caggtcgccg ggtgttccca ggaagaggaa gtaaatctgc aaccctgggg aggaccccaa 7740  
ctcacctggg aatgaggcaa attgcattt cttgctccct atgaatcactt ccagagggtt 7800  
gccttgcctt ggctgaggga catgtactgc ctctcatcta gaatttattt tccttagcact 7860  
tcaccacctc cttcatctt tccttcaaca ataaaccctg accaaatgt tcaaaaaaaa 7920

tataaaaaaag accagtccaa gcttattccc ttttagtgagg tt

7962

<210> 16  
<211> 1373  
<212> DNA  
<213> *Homo sapiens*

<220>  
<221> misc\_feature  
<223> Incyte Clone No: 2195418

```

<400> 16
cagccgggca gccgcttccc gcccccgacg aggagccggt gcgagcggag cagagccgag . 60
gtcggggcgc gaggcgagcc ggctgagcgg ggcggcagct cccgcacatgg cccgaaacac 120
gctgtctcg cgcttccgccc gggtgacat cgacgaattt gacgagaaca aatttgtgaa 180
cgagcaggag gaggcgccgg cggcgccggc ggagccaggc cccgaccggc gcgagggtgaa 240
cgggctctg cgccaagggg acatgttccg ggcattccat gcagccttgc ggaactctcc 300
cgtcaacacc aagaatcaag ctgtgaagga gggagccca ggcgttggc tgaaaatgtc 360
cacaacttc aagagcagtg agattgagca ggctgtcga tcactggaca gaaacggcgt 420
tgacttgttta atgaagtaca ttataaagg ctgttggaaa gggatggcggc cccacagaaa atagcagcgc 480
agtgttactc cagtggcacg aaaaggcctt agcagtagga ggactaggct ccattataag 540
agtcttaca gcaagaaaaga ctgtttaaaaaaa aaaataaaaaa gactcatgtt accttgagaa 600
gaattcttgg a tggccaggct ggtgaagaaag ggattgacaa tggaccatct tccttaggaac 660
tcccaagttaa actatttca gacatgtatc tgctgaaatg tattttttt tcaagggtgga 720
ggggaaaatc gtctgttcc taaatccgtt ttaggatctg atagttctatg ctttgttctc 780
cgagtactgc agaactgaca ttttgcggc ctaccagcgt ggcggctgg tttggtcaga 840
tgcacctgtg tgcaactgggg gagggtatgtt ttgggcaggc gcagatccaa gggctgtgt 900
aaacgggaga gcttgtgtt ttgaagtggaaa aaaaaaccca agagttgtt cagacatct 960
gtcttccag agaagggtggc cactcttggg ctcatgttta agtgctgtcgt gcatcaataa 1020
agctcttggc ttatttagtc atacatgtgc gtgttggcgt tttgtatgtaaa aaaaaatgtt 1080
aatgaatggg atggatataatg atgagatgc atgttgtt cccggaaaccc gatgtggaaag 1140
gagtagacct gtgtccctgt tgacccccc ctgggagcgc gcatggcaat ccacaggccc 1200
tctgccccag gacgccagcc tcggcctcgtt agctggccggc tgctgcagag aggtgtttgc 1260
tgaataaact atttattgtt tcttatttctt ttgatttgc tgtaattaaat ttggagcctt 1320
attnaattaa tttataaaatg tgccaaacat ttaataattt aaaaaaaaaaaa aaa 1373

```

<210> 17  
<211> 151  
<212> PRT  
<213> *Homo sapiens*

<220>  
<221> misc\_feature  
<223> GenBank ID No: q2282042

```

<400> 17
Met Ser Lys Asn Thr Val Ser Ser Ala Arg Phe Arg Lys Val Asp
      1           5           10          15
Val Asp Glu Tyr Asp Glu Asn Lys Phe Val Asp Glu Glu Asp Gly
      20          25          30
Gly Asp Gly Gln Ala Gly Pro Asp Glu Gly Glu Val Asp Ser Cys
      35          40          45
Leu Arg Gln Gly Asn Met Thr Ala Ala Leu Gln Ala Ala Leu Lys
      50          55          60
Asn Pro Pro Ile Asn Thr Lys Ser Gln Ala Val Lys Asp Arg Ala
      65          70          75
Gly Ser Ile Val Leu Lys Val Leu Ile Ser Phe Lys Ala Asn Asp
      80          85          90
Ile Glu Lys Ala Val Gln Ser Leu Asp Lys Asn Gly Val Asp Leu
      95         100         105
Leu Met Lys Tyr Ile Tyr Lys Gly Phe Glu Ser Pro Ser Asp Asn

```

	110	115	120											
Ser	Ser	Ala	Met	Leu	Leu	Gln	Trp	His	Glu	Lys	Ala	Leu	Ala	Ala
														135
														140
Gly	Gly	Val	Gly	Ser	Ile	Val	Arg	Val	Leu	Thr	Ala	Arg	Lys	Thr
														145
														150
Val														

**FOR THE PURPOSES OF INFORMATION ONLY**

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav	TM	Turkmenistan
BF	Burkina Faso	GR	Greece		Republic of Macedonia	TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's	NZ	New Zealand		
CM	Cameroon		Republic of Korea	PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakhstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		